Sequence Listing

<110> Kureha Chemical Industry Co., Ltd.

<120> Novel Proteins and Novel Genes Encoding the Same

<130> KRH-647

<150> JP 2000-042933
<151> 2000-02-21

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<212> DNA
<213> Homo sapiens

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<222> (37)..(1482)

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aca gaa agc ttt gcc aca gca atc cat ggc ttg aaa gtg gga cac ctg 102
Thr Glu Ser Phe Ala Thr Ala Ile His Gly Leu Lys Val Gly His Leu
10 15 20

aca gat cgt gtt att cag agg agc aag agg atg att cta gac act ctg 150
Thr Asp Arg Val Ile Gln Arg Ser Lys Arg Met Ile Leu Asp Thr Leu
25 30 35

ggt gct ggg ttc ctg gga acc act acg gaa gtg ttt cac ata gcc agc 198
Gly Ala Gly Phe Leu Gly Thr Thr Thr Glu Val Phe His Ile Ala Ser
40 45 50

caa tat agc aag atc tac agt tcc aac ata tcc agc act gta tgg ggt 246
Gln Tyr Ser Lys Ile Tyr Ser Ser Asn Ile Ser Ser Thr Val Trp Gly
55 60 65 70

cag cca gac atc agg ctc ccg ccc aca tat gct gct ttt gtg aac ggt 294
Gln Pro Asp Ile Arg Leu Pro Pro Thr Tyr Ala Ala Phe Val Asn Gly
75 80 85

gtg gct att cac tcc atg gat ttt gat gac acg tgg cac cct gcc acc 342
Val Ala Ile His Ser Met Asp Phe Asp Asp Thr Trp His Pro Ala Thr
90 95 100

cac cct tct ggg gct gtc ctt cct gtc ctc aca gct tta gca gaa gcc 390
His Pro Ser Gly Ala Val Leu Pro Val Leu Thr Ala Leu Ala Glu Ala
105 110 115

ctg cca agg agt cca aag ttt tct ggc ctt gac ctg ctg ctg gct ttc 438
Leu Pro Arg Ser Pro Lys Phe Ser Gly Leu Asp Leu Leu Leu Ala Phe
120 125 130

aat gtt ggt att gaa gtg caa ggc cga tta ctg cat ttc gcc aag gag 486
Asn Val Gly Ile Glu Val Gln Gly Arg Leu Leu His Phe Ala Lys Glu
135 140 145 150

gcc aat gac atg cca aag aga ttc cat ccc cct tcc gtg gta gga acg 534
Ala Asn Asp Met Pro Lys Arg Phe His Pro Pro Ser Val Val Gly Thr
155 160 165

ttg ggt agt gct gct gct gca tcc aag ttt tta gga ctt agc tcg aca 582
Leu Gly Ser Ala Ala Ala Ala Ser Lys Phe Leu Gly Leu Ser Ser Thr
170 175 180

aag tgc cga gaa gct ctg gcc att gct gtt tcc cat gct ggg gca ccc 630
Lys Cys Arg Glu Ala Leu Ala Ile Ala Val Ser His Ala Gly Ala Pro
185 190 195

atg gcc aat gct gcc acc cag acc aag ccc ctc cac att ggc aat gct 678

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Met Ala Asn Ala Ala Thr Gln Thr Lys Pro Leu His Ile Gly Asn Ala
    200                 205                 210

gcc aag cat ggg ata gaa gct gca ttt ttg gca atg ttg ggt ctc caa   726
Ala Lys His Gly Ile Glu Ala Ala Phe Leu Ala Met Leu Gly Leu Gln
215                 220                 225                 230

gga aac aag cag gtc ttg gac ttg gag gca gga ttt ggg gcc ttt tat   774
Gly Asn Lys Gln Val Leu Asp Leu Glu Ala Gly Phe Gly Ala Phe Tyr
                235                 240                 245

gcc aac tat tcc cca aaa gtc ctt cca agc ata gct tcc tac agt tgg   822
Ala Asn Tyr Ser Pro Lys Val Leu Pro Ser Ile Ala Ser Tyr Ser Trp
            250                 255                 260

ctg ctg gac cag cag gac gtg gcc ttt aag cgt ttt cct gca cat tta   870
Leu Leu Asp Gln Gln Asp Val Ala Phe Lys Arg Phe Pro Ala His Leu
        265                 270                 275

tct acc cac tgg gtg gca gac gca gct gca tct gtg aga aag cac ctt   918
Ser Thr His Trp Val Ala Asp Ala Ala Ala Ser Val Arg Lys His Leu
    280                 285                 290

gta gca gag aga gcc ctg ctt cca act gac tac att aag aga att gtg   966
Val Ala Glu Arg Ala Leu Leu Pro Thr Asp Tyr Ile Lys Arg Ile Val
295                 300                 305                 310

ctc agg ata cca aat gtc cag tat gta aac agg ccc ttt cca gtt tcg   1014
Leu Arg Ile Pro Asn Val Gln Tyr Val Asn Arg Pro Phe Pro Val Ser
                315                 320                 325

gag cat gaa gcc cgt cat tca ttc cag tat gtg gcc tgt gcc atg ctg   1062
Glu His Glu Ala Arg His Ser Phe Gln Tyr Val Ala Cys Ala Met Leu
            330                 335                 340

ctt gat ggt ggc atc act gtc ccc tca ttc cat gaa tgc cag atc aac   1110
Leu Asp Gly Gly Ile Thr Val Pro Ser Phe His Glu Cys Gln Ile Asn
        345                 350                 355
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agg cca cag gtg aga gag ctg ctc agt aag gtg gag ctg gag tac cct   1158
Arg Pro Gln Val Arg Glu Leu Leu Ser Lys Val Glu Leu Glu Tyr Pro
    360                 365                 370

ccg gac aac ttg cca agc ttc aac ata ctg tac tgt gaa ata agt gtc   1206
Pro Asp Asn Leu Pro Ser Phe Asn Ile Leu Tyr Cys Glu Ile Ser Val
375                 380                 385                 390

acc ctc aag gat gga gcc acc ttc aca gat cgc tct gat acc ttc tat   1254
Thr Leu Lys Asp Gly Ala Thr Phe Thr Asp Arg Ser Asp Thr Phe Tyr
                395                 400                 405

ggg cac tgg aga aaa cca ctg agc cag gag gac cta gag gaa aag ttc   1302
Gly His Trp Arg Lys Pro Leu Ser Gln Glu Asp Leu Glu Glu Lys Phe
            410                 415                 420

aga gcc aat gcc tcc aag atg ctg tcc tgg gac aca gtg gaa agc ctt   1350
Arg Ala Asn Ala Ser Lys Met Leu Ser Trp Asp Thr Val Glu Ser Leu
        425                 430                 435

ata aag ata gtc aaa aat cta gaa gac cta gaa gac tgt tct gtg tta   1398
Ile Lys Ile Val Lys Asn Leu Glu Asp Leu Glu Asp Cys Ser Val Leu
    440                 445                 450

act aca ctt ctc aaa gga ccc tct cca cca gag gta gct tca aac tct   1446
Thr Thr Leu Leu Lys Gly Pro Ser Pro Pro Glu Val Ala Ser Asn Ser
455                 460                 465                 470

cca gca tgt aat aat tct atc aca aat ctc tcc tgaggcttac caacatctaa 1499
Pro Ala Cys Asn Asn Ser Ile Thr Asn Leu Ser
                475                 480

atgactttgc atttggggag attcaatgat ttggtttgta aagcaagggt ctgctgcttg 1559

gttttcccag gaaaaatgaa caaagatgga gagagtccag aaacagaact acatatatct 1619

ggaaggagcc ttctcctgaa aattttgcag gacagttcca cttacctaaa tcaagatgaa 1679
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acacacacac aaaaatgagt ttgtaagcat tcacaagggt gaaattcaac tcacctgtga 1739

tttacttata aaattaatct cttcatagga attatgtgtg gacttcatga gcctcaaggt 1799

tttagaggga tgtgaacctg catgtatatt ttctgacagt ggagagggct ctggtgcatt 1859

gtgtcaccaa cagatctcct agaccatggc ttattaccaa gccctccaca gtgcaagggg 1919

tgctactggg gaatgggtgg gtttaaatcc tgcctctgcc attcactaga tgtagccttg 1979

agcatgttac cattagccct ctgcctcagt ttccctattt gtcaagccga agtaaaaagc 2039

agtctggaaa aatcgcattt tggctctaga acccatggtc ttaagcactg caatatatca 2099

cctttcagta taaaaatatt tgaatcagag ttgcaataaa gaatgaaaag gaaaaaagag 2159

aagtaaaaaa aaaaaaaaaa a 2180

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<212> PRT
<213> Homo sapiens

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 1               5                  10                  15

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            20                  25                  30

Met Ile Leu Asp Thr Leu Gly Ala Gly Phe Leu Gly Thr Thr Thr Glu
        35                  40                  45

Val Phe His Ile Ala Ser Gln Tyr Ser Lys Ile Tyr Ser Ser Asn Ile
    50                  55                  60
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Ser Ser Thr Val Trp Gly Gln Pro Asp Ile Arg Leu Pro Pro Thr Tyr
65 70 75 80

Ala Ala Phe Val Asn Gly Val Ala Ile His Ser Met Asp Phe Asp Asp
85 90 95

Thr Trp His Pro Ala Thr His Pro Ser Gly Ala Val Leu Pro Val Leu
100 105 110

Thr Ala Leu Ala Glu Ala Leu Pro Arg Ser Pro Lys Phe Ser Gly Leu
115 120 125

Asp Leu Leu Leu Ala Phe Asn Val Gly Ile Glu Val Gln Gly Arg Leu
130 135 140

Leu His Phe Ala Lys Glu Ala Asn Asp Met Pro Lys Arg Phe His Pro
145 150 155 160

Pro Ser Val Val Gly Thr Leu Gly Ser Ala Ala Ala Ala Ser Lys Phe
165 170 175

Leu Gly Leu Ser Ser Thr Lys Cys Arg Glu Ala Leu Ala Ile Ala Val
180 185 190

Ser His Ala Gly Ala Pro Met Ala Asn Ala Ala Thr Gln Thr Lys Pro
195 200 205

Leu His Ile Gly Asn Ala Ala Lys His Gly Ile Glu Ala Ala Phe Leu
210 215 220

Ala Met Leu Gly Leu Gln Gly Asn Lys Gln Val Leu Asp Leu Glu Ala
225 230 235 240

Gly Phe Gly Ala Phe Tyr Ala Asn Tyr Ser Pro Lys Val Leu Pro Ser
245 250 255

Ile Ala Ser Tyr Ser Trp Leu Leu Asp Gln Gln Asp Val Ala Phe Lys
260 265 270

Arg Phe Pro Ala His Leu Ser Thr His Trp Val Ala Asp Ala Ala Ala
275 280 285

Ser Val Arg Lys His Leu Val Ala Glu Arg Ala Leu Leu Pro Thr Asp
290 295 300

Tyr Ile Lys Arg Ile Val Leu Arg Ile Pro Asn Val Gln Tyr Val Asn
305 310 315 320

Arg Pro Phe Pro Val Ser Glu His Glu Ala Arg His Ser Phe Gln Tyr
325 330 335

Val Ala Cys Ala Met Leu Leu Asp Gly Gly Ile Thr Val Pro Ser Phe
340 345 350

His Glu Cys Gln Ile Asn Arg Pro Gln Val Arg Glu Leu Leu Ser Lys
355 360 365

Val Glu Leu Glu Tyr Pro Pro Asp Asn Leu Pro Ser Phe Asn Ile Leu
370 375 380

Tyr Cys Glu Ile Ser Val Thr Leu Lys Asp Gly Ala Thr Phe Thr Asp
385 390 395 400

Arg Ser Asp Thr Phe Tyr Gly His Trp Arg Lys Pro Leu Ser Gln Glu
405 410 415

Asp Leu Glu Glu Lys Phe Arg Ala Asn Ala Ser Lys Met Leu Ser Trp
420 425 430

Asp Thr Val Glu Ser Leu Ile Lys Ile Val Lys Asn Leu Glu Asp Leu
435 440 445

Glu Asp Cys Ser Val Leu Thr Thr Leu Leu Lys Gly Pro Ser Pro Pro
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Glu Val Ala Ser Asn Ser Pro Ala Cys Asn Asn Ser Ile Thr Asn Leu

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<213> Homo sapiens

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actcc atg gat ttt gat gac acg tgg cac cct gcc acc cac cct tct ggg 170
Met Asp Phe Asp Asp Thr Trp His Pro Ala Thr His Pro Ser Gly
1 5 10 15

gct gtc ctt cct gtc ctc aca gct tta gca gaa gcc ctg cca agg agt 218
Ala Val Leu Pro Val Leu Thr Ala Leu Ala Glu Ala Leu Pro Arg Ser
20 25 30

cca aag ttt tct ggc ctt gac ctg ctg ctg gct ttc aat gtt ggt att 266
Pro Lys Phe Ser Gly Leu Asp Leu Leu Leu Ala Phe Asn Val Gly Ile
35 40 45

gaa gtg caa ggc cga tta ctg cat ttc gcc aag gag gcc aat gac atg 314
Glu Val Gln Gly Arg Leu Leu His Phe Ala Lys Glu Ala Asn Asp Met
50 55 60

cca aag aga ttc cat ccc cct tcc gtg gta gga acg ttg ggt agt gct 362
Pro Lys Arg Phe His Pro Pro Ser Val Val Gly Thr Leu Gly Ser Ala
65 70 75

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gct gct gca tcc aag ttt tta gga ctt agc tcg aca aag tgc cga gaa   410
Ala Ala Ala Ser Lys Phe Leu Gly Leu Ser Ser Thr Lys Cys Arg Glu
 80                  85                  90                  95

gct ctg gcc att gct gtt tcc cat gct ggg gca ccc atg gcc aat gct   458
Ala Leu Ala Ile Ala Val Ser His Ala Gly Ala Pro Met Ala Asn Ala
                100                 105                 110

gcc acc cag acc aag ccc ctc cac att ggc aat gct gcc aag cat ggg   506
Ala Thr Gln Thr Lys Pro Leu His Ile Gly Asn Ala Ala Lys His Gly
            115                 120                 125

ata gaa gct gca ttt ttg gca atg ttg ggt ctc caa gga aac aag cag   554
Ile Glu Ala Ala Phe Leu Ala Met Leu Gly Leu Gln Gly Asn Lys Gln
        130                 135                 140

gtc ttg gac ttg gag gca gga ttt ggg gcc ttt tat gcc aac tat tcc   602
Val Leu Asp Leu Glu Ala Gly Phe Gly Ala Phe Tyr Ala Asn Tyr Ser
    145                 150                 155

cca aaa gtc ctt cca agc ata gct tcc tac agt tgg ctg ctg gac cag   650
Pro Lys Val Leu Pro Ser Ile Ala Ser Tyr Ser Trp Leu Leu Asp Gln
160                 165                 170                 175

cag gac gtg gcc ttt aag cgt ttt cct gca cat tta tct acc cac tgg   698
Gln Asp Val Ala Phe Lys Arg Phe Pro Ala His Leu Ser Thr His Trp
                180                 185                 190

gtg gca gac gca gct gca tct gtg aga aag cac ctt gta gca gag aga   746
Val Ala Asp Ala Ala Ala Ser Val Arg Lys His Leu Val Ala Glu Arg
            195                 200                 205

gcc ctg ctt cca act gac tac att aag aga att gtg ctc agg ata cca   794
Ala Leu Leu Pro Thr Asp Tyr Ile Lys Arg Ile Val Leu Arg Ile Pro
        210                 215                 220

aat gtc cag tat gta aac agg ccc ttt cca gtt tcg gag cat gaa gcc   842
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Asn Val Gln Tyr Val Asn Arg Pro Phe Pro Val Ser Glu His Glu Ala
    225                 230                 235

cgt cat tca ttc cag tat gtg gcc tgt gcc atg ctg ctt gat ggt ggc  890
Arg His Ser Phe Gln Tyr Val Ala Cys Ala Met Leu Leu Asp Gly Gly
240                 245                 250                 255

atc act gtc ccc tca ttc cat gaa tgc cag atc aac agg cca cag gtg  938
Ile Thr Val Pro Ser Phe His Glu Cys Gln Ile Asn Arg Pro Gln Val
                260                 265                 270

aga gag ctg ctc agt aag gtg gag ctg gag tac cct ccg gac aac ttg  986
Arg Glu Leu Leu Ser Lys Val Glu Leu Glu Tyr Pro Pro Asp Asn Leu
            275                 280                 285

cca agc ttc aac ata ctg tac tgt gaa ata agt gtc acc ctc aag gat 1034
Pro Ser Phe Asn Ile Leu Tyr Cys Glu Ile Ser Val Thr Leu Lys Asp
        290                 295                 300

gga gcc acc ttc aca gat cgc tct gat acc ttc tat ggg cac tgg aga 1082
Gly Ala Thr Phe Thr Asp Arg Ser Asp Thr Phe Tyr Gly His Trp Arg
    305                 310                 315

aaa cca ctg agc cag gag gac cta gag gaa aag ttc aga gcc aat gcc 1130
Lys Pro Leu Ser Gln Glu Asp Leu Glu Glu Lys Phe Arg Ala Asn Ala
320                 325                 330                 335

tcc aag atg ctg tcc tgg gac aca gtg gaa agc ctt ata aag ata gtc 1178
Ser Lys Met Leu Ser Trp Asp Thr Val Glu Ser Leu Ile Lys Ile Val
                340                 345                 350

aaa aat cta gaa gac cta gaa gac tgt tct gtg tta act aca ctt ctc 1226
Lys Asn Leu Glu Asp Leu Glu Asp Cys Ser Val Leu Thr Thr Leu Leu
            355                 360                 365

aaa gga ccc tct cca cca gag gta gct tca aac tct cca gca tgt aat 1274
Lys Gly Pro Ser Pro Pro Glu Val Ala Ser Asn Ser Pro Ala Cys Asn
        370                 375                 380
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aat tct atc aca aat ctc tcc tgaggcttac caacatctaa atgactttgc 1325
Asn Ser Ile Thr Asn Leu Ser
385 390

atttggggag attcaatgat ttggtttgta aagcaagggt ctgctgcttg gttttcccag 1385

gaaaaatgaa caaagatgga gagagtccag aaacagaact acatatatct ggaaggagcc 1445

ttctcctgaa aattttgcag gacagttcca cttacctaaa tcaagatgaa acacacacac 1505

aaaaatgagt ttgtaagcat tcacaagggt gaaattcaac tcacctgtga tttacttata 1565

aaattaatct cttcatagga attatgtgtg gacttcatga gcctcaaggt tttagaggga 1625

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cagatctcct agaccatggc ttattaccaa gccctccaca gtgcaagggg tgctactggg 1745

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aatcgcattt tggctctaga acccatggtc ttaagcactg caatatatca cctttcagta 1925

taaaaatatt tgaatcagag ttgcaataaa aaaaaaaaaa aaaaa 1970

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<212> PRT
<213> Homo sapiens

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            35                  40                  45

Val Gln Gly Arg Leu Leu His Phe Ala Lys Glu Ala Asn Asp Met Pro
        50                  55                  60

Lys Arg Phe His Pro Pro Ser Val Val Gly Thr Leu Gly Ser Ala Ala
65                  70                  75                  80

Ala Ala Ser Lys Phe Leu Gly Leu Ser Ser Thr Lys Cys Arg Glu Ala
                85                  90                  95

Leu Ala Ile Ala Val Ser His Ala Gly Ala Pro Met Ala Asn Ala Ala
            100                 105                 110

Thr Gln Thr Lys Pro Leu His Ile Gly Asn Ala Ala Lys His Gly Ile
        115                 120                 125

Glu Ala Ala Phe Leu Ala Met Leu Gly Leu Gln Gly Asn Lys Gln Val
    130                 135                 140

Leu Asp Leu Glu Ala Gly Phe Gly Ala Phe Tyr Ala Asn Tyr Ser Pro
145                 150                 155                 160

Lys Val Leu Pro Ser Ile Ala Ser Tyr Ser Trp Leu Leu Asp Gln Gln
                165                 170                 175

Asp Val Ala Phe Lys Arg Phe Pro Ala His Leu Ser Thr His Trp Val
            180                 185                 190

Ala Asp Ala Ala Ala Ser Val Arg Lys His Leu Val Ala Glu Arg Ala
        195                 200                 205

Leu Leu Pro Thr Asp Tyr Ile Lys Arg Ile Val Leu Arg Ile Pro Asn
    210                 215                 220
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Val Gln Tyr Val Asn Arg Pro Phe Pro Val Ser Glu His Glu Ala Arg
225 230 235 240

His Ser Phe Gln Tyr Val Ala Cys Ala Met Leu Leu Asp Gly Gly Ile
245 250 255

Thr Val Pro Ser Phe His Glu Cys Gln Ile Asn Arg Pro Gln Val Arg
260 265 270

Glu Leu Leu Ser Lys Val Glu Leu Glu Tyr Pro Pro Asp Asn Leu Pro
275 280 285

Ser Phe Asn Ile Leu Tyr Cys Glu Ile Ser Val Thr Leu Lys Asp Gly
290 295 300

Ala Thr Phe Thr Asp Arg Ser Asp Thr Phe Tyr Gly His Trp Arg Lys
305 310 315 320

Pro Leu Ser Gln Glu Asp Leu Glu Glu Lys Phe Arg Ala Asn Ala Ser
325 330 335

Lys Met Leu Ser Trp Asp Thr Val Glu Ser Leu Ile Lys Ile Val Lys
340 345 350

Asn Leu Glu Asp Leu Glu Asp Cys Ser Val Leu Thr Thr Leu Leu Lys
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370 375 380

Ser Ile Thr Asn Leu Ser
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Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu Val
5 10 15

gtg ttc atg act gtg gcg gcg ggt gga gcc tca tct ttc gct gtg tat 154
Val Phe Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val Tyr
20 25 30

tct ctt tgg aaa acc gat gtg atc ctt gat cga aaa aaa aat cca gaa 202
Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro Glu
35 40 45

cct tgg gaa act gtg gac cct act gta cct caa aag ctt ata aca atc 250
Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr Ile
50 55 60 65

aac caa caa tgg aaa ccc att gaa gag ttg caa aat gtc caa agg gtg 298
Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg Val
70 75 80

acc aaa tgacgagccc tcgcctcttt cttctgaaga gtactctata aatctagtgg 354
Thr Lys

aaacatttct gcacaaacta gattctggac accagtgtgc ggaaatgctt ctgctacatt 414

tttagggttt gtctacattt tttgggctct ggataaggaa ttaaaggagt gcagcaataa 474

ctgcactgtc taaaagtttg tgcttatttt cttgtaaatt tgaatattgc atattgaaat 534

ttttgtttat gatctatgaa tgtttttctt aaaatttaca aagctttgta aattagattt 594

tctttaataa aatgccattt gtgcaagatt tctcaaagaa aaaaaaaaaa aaaaaaaa 652

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<212> PRT
<213> Homo sapiens

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1 5 10 15

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20 25 30

Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro
35 40 45

Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr
50 55 60

Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg
65 70 75 80

Val Thr Lys

<210> 7
<211> 34
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<213> Artificial Sequence

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<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: NLG-2 reverse primer

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gtggaattct ttggtcaccc tttggacatt ttgc 34

<210> 9
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: NLG-1-1 forward primer

<400> 9
cacggatcct tctttacaac gaaatgatgc tcaag 35

<210> 10
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: NLG-1-1 reverse

primer

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